

SEQUENCE LISTING



<110> Yano, Tetsuya; Nomoto, tsuyoshi; Immura, Takeshi; Canon Kabushiki Kaisha

<120> DNA Fragment Carrying Toluene Monooxygenase Gene,
Recombinant Plasmid, Transformed Microorganism,
Method for Degrading Chlorinated Aliphatic Hydrocarbon
Compounds and Aromatic Compounds, and
Method for Environmental Remediation

<130> CFO13982US

<140> 09/430029

<141> 1999-10-29

<150> JP P1998-310801

<151> 1998-10-30

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 5828

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (234)..(443)

<223> tomK

<220>

<221> CDS

<222> (463)..(1455)

<223> tomL

<220>

<221> CDS

<222> (1495)..(1761)

<223> tomM



<220>
 <221> CDS
 <222> (1803)..(3350)
 <223> tomN

<220>
 <221> CDS
 <222> (3428)..(3781)
 <223> tomO

<220>
 <221> CDS
 <222> (3810)..(4871)
 <223> tomP

<220>
 <221> CDS
 <222> (4876)..(5229)
 <223> tomQ

<400> 1
 gatcatttca tcaaatgcgc tcgagcgggt tgctcaaatg atgaaaaagg ccaccggaca 60
 tgggtttcgg cacgatcgcc ggcgggcgtt ttccgttctg gttaaccgcc attgtgggtc 120
 gcgaaattta acttcgcgtc agggctttcc ctgaattatc gagattttt gctgcctggg 180
 tcgaacgtgg cacggatgct gcattgaagt ccggcatgga ggcgacacccg atc atg 236
 Met
 1
 aat cag cac ccc acc gat ctt tcc ccg ttc gat ccc ggc cgc aag tgc 284
 Asn Gln His Pro Thr Asp Leu Ser Pro Phe Asp Pro Gly Arg Lys Cys
 5 10 15
 gtc cgc gtg acc ggc acg aac gcg cgc ggc ttc gtc gaa ttc gag ctg 332
 Val Arg Val Thr Gly Thr Asn Ala Arg Gly Phe Val Glu Phe Glu Leu
 20 25 30
 tcg atc ggc ggc gcg ccg gaa ctg tgc gtc gag ctg acg ttg tct cct 380
 Ser Ile Gly Gly Ala Pro Glu Leu Cys Val Glu Leu Thr Leu Ser Pro
 35 40 45
 gcc gcc ttc gat gcg ttc tgc cgc gaa cag cag gtc acg cgg ctc gac 428

Ala Ala Phe Asp Ala Phe Cys Arg Glu Gln Gln Val Thr Arg Leu Asp 50 55 60 65
 gtc gaa gcg aac cca tgacctttag gaggcaagaa gtg acc atc gag ctg aag 480
 Val Glu Ala Asn Pro Met Thr Ile Glu Leu Lys 70 75
 aca gtc gac atc aag ccg ctc cgg cac acc ttt gcg cat gtc gcg cag 528
 Thr Val Asp Ile Lys Pro Leu Arg His Thr Phe Ala His Val Ala Gln 80 85 90
 aac atc ggc ggc gac aag acg gcg acg cgc tac cag gaa ggc atg atg 576
 Asn Ile Gly Gly Asp Lys Thr Ala Thr Arg Tyr Gln Glu Gly Met Met 95 100 105
 ggc gcg cag ccc cag gag aac ttc cat tac cgg ccg acc tgg gac ccg 624
 Gly Ala Gln Pro Gln Glu Asn Phe His Tyr Arg Pro Thr Trp Asp Pro 110 115 120
 gac tac gag atc ttc gat ccg tcg cgc tcg gcg atc cgg atg gcg aac 672
 Asp Tyr Glu Ile Phe Asp Pro Ser Arg Ser Ala Ile Arg Met Ala Asn 125 130 135 140
 tgg tac gcg ttg aag gat ccg cgc cag ttc tac tac gcg tcg tgg gcg 720
 Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe Tyr Tyr Ala Ser Trp Ala 145 150 155
 acc acg ccg gcg cgc cag cag gat gcg atg gag tcg aac ttc gag ttc 768
 Thr Thr Arg Ala Arg Gln Gln Asp Ala Met Glu Ser Asn Phe Glu Phe 160 165 170
 gtc gaa tcg cgc ccg atg atc ggc ctg atg cgc gac gac gtg gcc gcg 816
 Val Glu Ser Arg Arg Met Ile Gly Leu Met Arg Asp Asp Val Ala Ala 175 180 185
 cgg gcg ctc gac gtg ctg gtg ccg ctg cgc cac gcc gcg tgg ggc gcg 864
 Arg Ala Leu Asp Val Leu Val Pro Leu Arg His Ala Ala Trp Gly Ala 190 195 200
 aac atg aac aac gcg cag atc tgc gcg ctc ggc tac ggc acg gtg ttc 912
 Asn Met Asn Asn Ala Gln Ile Cys Ala Leu Gly Tyr Gly Thr Val Phe 205 210 215 220
 acc gcg ccc gcg atg ttc cat gcg atg gac aac ctc ggc gtc gcg caa 960

Thr Ala Pro Ala Met Phe His Ala Met Asp Asn Leu Gly Val Ala Gln
 225 230 235

tac ctc acg cgt ctc gcg ctc gcg atg gcc gag ccc gac gtg ctg gag 1008
 Tyr Leu Thr Arg Leu Ala Leu Ala Met Ala Glu Pro Asp Val Leu Glu
 240 245 250

gcg gcc aag gcg acc tgg acc cgc gac gcc gcc tgg cag ccg ctg cgc 1056
 Ala Ala Lys Ala Thr Trp Thr Arg Asp Ala Ala Trp Gln Pro Leu Arg
 255 260 265

cgc tac gtc gag gac acg ctg gtc gcc gat ccg gtc gag ctg ttc 1104
 Arg Tyr Val Glu Asp Thr Leu Val Val Ala Asp Pro Val Glu Leu Phe
 270 275 280

atc gcg cag aac ctc gcg ctc gac ggc ctg ctg tat ccg ctc gtc tac 1152
 Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu Leu Tyr Pro Leu Val Tyr
 285 290 295 300

gac cgc ttc gtc gac gaa cgg atc gcg ctc gaa ggc ggc tcg gca gtc 1200
 Asp Arg Phe Val Asp Glu Arg Ile Ala Leu Glu Gly Gly Ser Ala Val
 305 310 315

gcg atg ctg acc gcg ttc atg ccc gaa tgg cac acc gag tcg aac cgc 1248
 Ala Met Leu Thr Ala Phe Met Pro Glu Trp His Thr Glu Ser Asn Arg
 320 325 330

ATC
 tgg atc gac gcg gtc gtg aag acg atg gcc gaa tcc gac gac aac 1296
 Trp Ile Asp Ala Val Val Lys Thr Met Ala Ala Glu Ser Asp Asp Asn
 335 340 345

cgc gcg ctg ctc gcc cgc tgg aca cgc gac tgg tcc gcg cgc gcc gag 1344
 Arg Ala Leu Leu Ala Arg Trp Thr Arg Asp Trp Ser Ala Arg Ala Glu
 350 355 360

gcg gca ctg gca ccc gtg gcg gca cgc gcg ctg cag gat gcc ggg cgc 1392
 Ala Ala Leu Ala Pro Val Ala Ala Arg Ala Leu Gln Asp Ala Gly Arg
 365 370 375 380

gcg gcg ctc gac gaa gtg cgc gag cag ttc cac gca cgc gcg gcc agg 1440
 Ala Ala Leu Asp Glu Val Arg Glu Gln Phe His Ala Arg Ala Ala Arg
 385 390 395

ctc ggc atc gcg ctc tgacgacggg aatcctccct taacccaagg aatgccagc 1494

Leu Gly Ile Ala Leu
 400

atg tcc aac gta ttc atc gcc ttt cag gcc aat gag gac tcc aga ccg 1542
 Met Ser Asn Val Phe Ile Ala Phe Gln Ala Asn Glu Asp Ser Arg Pro
 405 410 415

atc gtg gat gcg atc gtc gcc gac aac ccg cgc gcg gtg gtg gtc gag 1590
 Ile Val Asp Ala Ile Val Ala Asp Asn Pro Arg Ala Val Val Val Glu
 420 425 430

tcg ccc ggc atg gtc aag atc gac gcg ccg gac ccg ctg acg atc cgc 1638
 Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
 435 440 445

cgc gaa acg atc gag gaa ctg acc ggc acg cgc ttc gac ctg cag cag 1686
 Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
 450 455 460 465

ctc cag gtc aac ctg atc acg ctg tca ggc cac atc gac gag gac gac 1734
 Leu Gln Val Asn Leu Ile Thr Leu Ser Gly His Ile Asp Glu Asp Asp
 470 475 480

gac gag ttc acg ctg agc tgg tcg cac tgaacgcccgc gccacgcgca 1781
 Asp Glu Phe Thr Leu Ser Trp Ser His
 485 490

ccgacaacac cggagacacg a atg gac acg cca acg ctc aag aaa aaa ctc 1832
 Met Asp Thr Pro Thr Leu Lys Lys Lys Leu
 495 500

ggc ctg aag gac cgc tac gcg gca atg acg cgc ggc ctc ggc tgg gag 1880
 Gly Leu Lys Asp Arg Tyr Ala Ala Met Thr Arg Gly Leu Gly Trp Glu
 505 510 515

acg acc tac cag ccg atg gac aag gtc ttc ccg tac gac cgc tac gag 1928
 Thr Thr Tyr Gln Pro Met Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu
 520 525 530

ggc atc aag atc cac gac tgg gac aag tgg gtc gac ccg ttc cgc ctg 1976
 Gly Ile Lys Ile His Asp Trp Asp Lys Trp Val Asp Pro Phe Arg Leu
 535 540 545

acg atg gat gcg tac tgg aaa tac cag ggc gag aag gaa aag aag ctg 2024

Thr Met Asp Ala Tyr Trp Lys Tyr Gln Gly Glu Lys Lys Lys Leu
 550 555 560

tac gcg gtg atc gac gcg ttc acg cag aac aac gcg ttc ctc ggc gtg 2072
 Tyr Ala Val Ile Asp Ala Phe Thr Gln Asn Asn Ala Phe Leu Gly Val
 565 570 575 580

agc gac gcc cgc tac atc aac gcg ctg aag ctg ttc ctc cag ggc gtg 2120
 Ser Asp Ala Arg Tyr Ile Asn Ala Leu Lys Leu Phe Leu Gln Gly Val
 585 590 595

acg ccg ctc gaa tac ctc gcg cac cgc ggc ttc gcg cat gtc ggc cgg 2168
 Thr Pro Leu Glu Tyr Leu Ala His Arg Gly Phe Ala His Val Gly Arg
 600 605 610

cac ttc acc ggc gag ggc gcg cgc atc gcg tgc cag atg cag tcg atc 2216
 His Phe Thr Gly Glu Gly Ala Arg Ile Ala Cys Gln Met Gln Ser Ile
 615 620 625

gac gag ctg cgg cac tac cag acc gaa acg cat gcg atg tcg acg tac 2264
 Asp Glu Leu Arg His Tyr Gln Thr Glu Thr His Ala Met Ser Thr Tyr
 630 635 640

aac aag ttc ttc aac ggg ttc cat cac tcg aac cag tgg ttc gac cgc 2312
 Asn Lys Phe Phe Asn Gly Phe His His Ser Asn Gln Trp Phe Asp Arg
 645 650 655 660

gtg tgg tac ctg tcg gtg ccg aag tcg ttc ttc gag gac gcg tat tcg 2360
 Val Trp Tyr Leu Ser Val Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser
 665 670 675

tcg ggg ccg ttc gag ttc ctg acc gcg gtc acg ttc tcg ttc gaa tac 2408
 Ser Gly Pro Phe Glu Phe Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr
 680 685 690

gtg ctg acg aac ctg ctg ttc gtg ccg ttc atg tcg ggc gcc gcc tac 2456
 Val Leu Thr Asn Leu Leu Phe Val Pro Phe Met Ser Gly Ala Ala Tyr
 695 700 705

aac ggt gac atg tcg acc gtc acg ttc ggc ttc tcc gcg cag tcg gac 2504
 Asn Gly Asp Met Ser Thr Val Thr Phe Gly Phe Ser Ala Gln Ser Asp
 710 715 720

gaa tcg cgt cac atg acg ctc ggc atc gaa tgc atc aag ttc ctg ctc 2552

Glu Ser Arg His Met Thr Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu
 725 730 735 740

gaa cag gac ccg gac aac gtg ccg atc gtg cag cgc tgg atc gac aag 2600
 Glu Gln Asp Pro Asp Asn Val Pro Ile Val Gln Arg Trp Ile Asp Lys
 745 750 755

tgg ttc tgg cgc ggc tac ccg ctg acg ctg gtc gcg atg atg atg 2648
 Trp Phe Trp Arg Gly Tyr Arg Leu Leu Thr Leu Val Ala Met Met Met
 760 765 770

gac tac atg cag ccc aag cgc gtg atg agc tgg cgc gag tcg tgg gag 2696
 Asp Tyr Met Gln Pro Lys Arg Val Met Ser Trp Arg Glu Ser Trp Glu
 775 780 785

atg tac gcc gag cag aac ggc ggc gcg ctg ttc aag gat ctc gcg cgc 2744
 Met Tyr Ala Glu Gln Asn Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg
 790 795 800

tac ggc att cgc gag ccg aag ggc tgg cag gac gcc tgc gaa ggc aag 2792
 Tyr Gly Ile Arg Glu Pro Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys
 805 810 815 820

gat cac atc agc cac cag gcg tgg tcg acg ttc tac ggc ttc aac gcg 2840
 Asp His Ile Ser His Gln Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala
 825 830 835

gcc tcg gcg ttc cac acc tgg gtg ccg acc gaa gac gaa atg ggc tgg 2888
 Ala Ser Ala Phe His Thr Trp Val Pro Thr Glu Asp Glu Met Gly Trp
 840 845 850

ctg tcg gcg aag tat ccc gac tcg ttc gac cgc tac tac cgc ccg cgc 2936
 Leu Ser Ala Lys Tyr Pro Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg
 855 860 865

ttc gat cac tgg ggc gag cag gcc agg gcc ggc aac cgc ttc tac atg 2984
 Phe Asp His Trp Gly Glu Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met
 870 875 880

aag acg ctg ccg atg ctg tgc cag acg tgc cag atc ccg atg ctg ttc 3032
 Lys Thr Leu Pro Met Leu Cys Gln Thr Cys Gln Ile Pro Met Leu Phe
 885 890 895 900

acc gag ccg ggc aac ccg acg aag atc ggc gcg cgc gaa tcg aac tac 3080

Thr	Glu	Pro	Gly	Asn	Pro	Thr	Lys	Ile	Gly	Ala	Arg	Glu	Ser	Asn	Tyr	
																905
																910
																915
ctc	ggc	aac	aag	ttc	cac	ttc	tgc	agc	gac	cac	tgc	aag	gac	atc	ttc	3128
Leu	Gly	Asn	Lys	Phe	His	Phe	Cys	Ser	Asp	His	Cys	Lys	Asp	Ile	Phe	
																920
																925
																930
gat	cac	gag	ccg	cag	aaa	tac	gtg	cag	gcg	tgg	ctg	ccg	gtg	cac	cag	3176
Asp	His	Glu	Pro	Gln	Lys	Tyr	Val	Gln	Ala	Trp	Leu	Pro	Val	His	Gln	
																935
																940
																945
atc	cat	cag	ggc	aac	tgc	ttc	ccg	ccc	gat	gcg	gac	ccg	ggc	gcg	gag	3224
Ile	His	Gln	Gly	Asn	Cys	Phe	Pro	Pro	Asp	Ala	Asp	Pro	Gly	Ala	Glu	
																950
																955
																960
ggc	ttc	gat	ccg	ctc	gcc	gcg	gtg	ctc	gac	tac	tac	gcg	gtg	acg	atg	3272
Gly	Phe	Asp	Pro	Leu	Ala	Ala	Val	Leu	Asp	Tyr	Tyr	Ala	Val	Thr	Met	
																965
																970
																975
																980
ggc	cgc	gac	aac	ctc	gat	ttc	gac	ggc	tcg	gaa	gac	cag	aag	aac	ttc	3320
Gly	Arg	Asp	Asn	Leu	Asp	Phe	Asp	Gly	Ser	Glu	Asp	Gln	Lys	Asn	Phe	
																985
																990
																995
gcg	gcf	tgg	cgc	ggc	cag	gcc	acg	cgc	aac	tgacccgcaa	cgacaagcaa					3370
Ala	Ala	Trp	Arg	Gly	Gln	Ala	Thr	Arg	Asn							
																1000
																1005
tcttgcgag	ggcccgcgaa	gcccgcgtgc	gcgaacgcgg	gccgacacgga	gacaaac											3427
atg	gcc	gtc	atc	gcf	ctc	aaa	ccc	tac	gac	ttc	ccg	gtg	aag	gat	gcc	3475
Met	Ala	Val	Ile	Ala	Leu	Lys	Pro	Tyr	Asp	Phe	Pro	Val	Lys	Asp	Ala	
																1010
																1015
																1020
gtc	gag	aag	ttt	ccg	gcf	ccg	ctg	ctc	tac	gtg	tgc	tgg	gaa	aac	cat	3523
Val	Glu	Lys	Phe	Pro	Ala	Pro	Leu	Leu	Tyr	Val	Cys	Trp	Glu	Asn	His	
																1025
																1030
																1035
ctg	atg	ttc	ccg	gcf	ccg	ttc	tgc	ctg	ccg	ccg	ccc	gac	atg	ccg		3571
Leu	Met	Phe	Pro	Ala	Pro	Phe	Cys	Leu	Pro	Leu	Pro	Pro	Asp	Met	Pro	
																1040
																1045
																1050
ttc	ggc	gcf	ctg	gcc	ggc	gac	gtg	ctg	ccg	ccc	gtc	tac	ggc	tat	cac	3619
Phe	Gly	Ala	Leu	Ala	Gly	Asp	Val	Leu	Pro	Pro	Val	Tyr	Gly	Tyr	His	
																1055
																1060
																1065
																1070

ccc gac ttc gcg aag atc gac tgg gat cgc gtc gag tgg ttc cgg tcg	3667
Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser	
1075 1080 1085	
ggc gag ccg tgg gcg ccg gac ccg gcg aag agc ctg gcc ggc aac ggc	3715
Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly	
1090 1095 1100	
ctc ggg cac aag gac ctg atc agc ttc cgc acg ccc ggc ctc gac ggc	3763
Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp Gly	
1105 1110 1115	
ctc ggc ggc gcg agc ttc tgaccgccac gcggacgagc gaaccatc atg agc	3815
Leu Gly Gly Ala Ser Phe	
1120	Met Ser
1125	
cac caa ctt acc atc gag ccg ctg ggc gtc acg atc gag gtc gag gaa	3863
His Gln Leu Thr Ile Glu Pro Leu Gly Val Thr Ile Glu Val Glu Glu	
1130 1135 1140	
gga cag acg atg ctc gat gcc gcg ctg cgc cag ggc atc tac att ccg	3911
Gly Gln Thr Met Leu Asp Ala Ala Leu Arg Gln Gly Ile Tyr Ile Pro	
1145 1150 1155	
cac gcg tgc tgt cac ggg ctg tgc ggc acc tgc aag gtc gcc gtg ctc	3959
His Ala Cys Cys His Gly Leu Cys Gly Thr Cys Lys Val Ala Val Leu	
1160 1165 1170	
1 Acnt	
gac ggc gag acc gat ccc ggc gat gcg aac ccg ttc gcg ctg atg gat	4007
Asp Gly Glu Thr Asp Pro Gly Asp Ala Asn Pro Phe Ala Leu Met Asp	
1175 1180 1185 1190	
ttc gag cgc gag gaa ggc aag gcg ctc gcg tgc tgc gcg acg ctg cag	4055
Phe Glu Arg Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr Leu Gln	
1195 1200 1205	
gcc gac acc gtg atc gag gcc gac gtc gac gag gag ccg gat gcg gaa	4103
Ala Asp Thr Val Ile Glu Ala Asp Val Asp Glu Glu Pro Asp Ala Glu	
1210 1215 1220	
atc atc ccg gtc agg gac ttc gcg gcc gac gtc acg cgc atc gaa cag	4151
Ile Ile Pro Val Arg Asp Phe Ala Ala Asp Val Thr Arg Ile Glu Gln	
1225 1230 1235	

ctc acg ccg acc atc aag tcg atc cgc ctg aag ctg tcg cag ccg atc			4199
Leu Thr Pro Thr Ile Lys Ser Ile Arg Leu Lys Leu Ser Gln Pro Ile			
1240	1245	1250	
cgc ttc cag gcg ggc cag tac gtg cag ctc gag att ccc ggc ctc ggg			4247
Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly Leu Gly			
1255	1260	1265	1270
cag agc cgc gcg ttc tcg atc gcg aac gcg ccg gcc gac gtc gcg gcc			4295
Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val Ala Ala			
1275	1280	1285	
acc ggc gag atc gaa ctg aac gtg cgg cag gtg ccg ggc ggg ctc ggc			4343
Thr Gly Glu Ile Glu Leu Asn Val Arg Gln Val Pro Gly Gly Leu Gly			
1290	1295	1300	
acg ggc tac ctg cac gag caa ctg gcg acg ggc gag cgc gtg cgc ctg			4391
Thr Gly Tyr Leu His Glu Gln Leu Ala Thr Gly Glu Arg Val Arg Leu			
1305	1310	1315	
tcg ggc ccg tac ggc cgc ttc ttc gtg cgt cgc tcg gcc gcg cgg ccg			4439
Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala Arg Pro			
1320	1325	1330	
atg atc ttc atg gcc ggc ggg tcg ggg ctg tcg agc ccg cgc tcg atg			4487
Met Ile Phe Met Ala Gly Gly Ser Gly Leu Ser Ser Pro Arg Ser Met			
1335	1340	1345	1350
atc gcg gac ctg ctc gca agc ggc gtc acc gcg ccg atc acg ctg gtc			4535
Ile Ala Asp Leu Leu Ala Ser Gly Val Thr Ala Pro Ile Thr Leu Val			
1355	1360	1365	
<i>A</i> <i>cont</i> tac ggt cag cgc agc gcg cag gag ctc tac tac cac gac gaa ttc cgc			4583
Tyr Gly Gln Arg Ser Ala Gln Glu Leu Tyr Tyr His Asp Glu Phe Arg			
1370	1375	1380	
gcg ctg gcc gaa cgc cat ccg aac ttc acg tac gtg ccg gcg ctg tcc			4631
Ala Leu Ala Glu Arg His Pro Asn Phe Thr Tyr Val Pro Ala Leu Ser			
1385	1390	1395	
gaa ggc gca ccg cac gcg ggc gac gtc gcg caa ggg ttc gtg cac			4679
Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe Val His			
1400	1405	1410	

gac gtc gcg aag gca cat ttc ggc ggc gac ttc tcc ggg cac cag gcg	4727
Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His Gln Ala	
1415 1420 1425 1430	
tac ctg tgc ggg ccg ccc gcg atg atc gac gcg tgc atc acg acg ctg	4775
Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr Thr Leu	
1435 1440 1445	
atg cag ggg cgc ctg ttc gag cgc gac atc tat cac gag aag ttc atc	4823
Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys Phe Ile	
1450 1455 1460	
tcg gcg gcc gac gcg caa cag acg cgc agc ccg ctg ttc cgg cgg gtg	4871
Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg Arg Val	
1465 1470 1475	
tgac atg gac gcg ggc cgc gta tgc ggg acg gtc acg atc gcg cag acc	4920
Met Asp Ala Gly Arg Val Cys Gly Thr Val Thr Ile Ala Gln Thr	
1480 1485 1490	
gac gag cgc tat gcg tgc gtg tcc ggc gag tcg ctg ctg gcc ggc atg	4968
Asp Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met	
1495 1500 1505	
gcg aaa ctc ggc cgg cgc ggc att ccg gtc ggc tgc ctg aac ggc ggg	5016
Ala Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly	
1510 1515 1520 1525	
tgc ggc gtg tgc aag gtg cgc gtg ctg cgc ggt gcg gtg cgc aag ctc	5064
Cys Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu	
1530 1535 1540	
ggg ccg atc agc cgt gcc cat gtg agc gcg gaa gaa gag aac gac ggc	5112
Gly Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Glu Asn Asp Gly	
1545 1550 1555	
tac gcg ctt gcg tgc cgc gtc gtg ccg gac ggc gac gtc gaa ctc gaa	5160
Tyr Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu	
1560 1565 1570	
gtg gcc ggc cgg ctc agg aag ccg ttc ttc tgc ggc atg gca tgt gcc	5208
Val Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala	
1575 1580 1585	

A
Cont

ggc acg gcg gcg atc aac aag taaccaggag gagactcacc atgggtgtga 5259
Gly Thr Ala Ala Ile Asn Lys
1590 1595

tgcgtattgg tcatgtcagt ctgaaggta tggacatgga agcggcgctg cgtcattacg 5319
tacgcgtgct cggcatgcag gaaacgatgc gcgacgcggc gggcaacgtc tacctgaaat 5379
gctgggacga atgggacaag tattcgctga tcctgtcgcc gtccgatcag gcggggctca 5439
agcatgccgc ctacaaggta gaggcacgacg ccgatctgga tgcgtgcag cagcgcatcg 5499
aagcgtacgg gatcgccgacc gagatgctgc ccgaaggcgc gctgccggc gtcggccgccc 5559
aactgcggtt cctgctgccc agcggccatg aactgcggct gttcgcgaag aaggcgctgg 5619
tgggcaccgc ggtcggctcg ctgaaccccg atccgtggcc cgacgacatt ccgggctcgg 5679
ccgtgcactg gctcgaccac tgcctgctga tgtgcgaact gaacccggag gccggcgtga 5739
accgcgtcga ggagaacacg cgcttcatgg ccgagtgtct cgacttccat ctggccgagc 5799
aggtgatggc cggccgggc aacacgatc 5828

A
Cont'

<210> 2
<211> 70
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomK polypeptide

<400> 2

Met	Asn	Gln	His	Pro	Thr	Asp	Leu	Ser	Pro	Phe	Asp	Pro	Gly	Arg	Lys
1				5				10					15		
Cys	Val	Arg	Val	Thr	Gly	Thr	Asn	Ala	Arg	Gly	Phe	Val	Glu	Phe	Glu
				20					25				30		
Leu	Ser	Ile	Gly	Gly	Ala	Pro	Glu	Leu	Cys	Val	Glu	Leu	Thr	Leu	Ser
				35			40				45				
Pro	Ala	Ala	Phe	Asp	Ala	Phe	Cys	Arg	Glu	Gln	Gln	Val	Thr	Arg	Leu
				50		55				60					
Asp	Val	Glu	Ala	Asn	Pro										
	65				70										

<210> 3
<211> 331
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomL polypeptide

<400> 3
Met Thr Ile Glu Leu Lys Thr Val Asp Ile Lys Pro Leu Arg His Thr
1 5 10 15
Phe Ala His Val Ala Gln Asn Ile Gly Gly Asp Lys Thr Ala Thr Arg
20 25 30
Tyr Gln Glu Gly Met Met Gly Ala Gln Pro Gln Glu Asn Phe His Tyr
35 40 45
Arg Pro Thr Trp Asp Pro Asp Tyr Glu Ile Phe Asp Pro Ser Arg Ser
50 55 60
Ala Ile Arg Met Ala Asn Trp Tyr Ala Leu Lys Asp Pro Arg Gln Phe
65 70 75 80
Tyr Tyr Ala Ser Trp Ala Thr Thr Arg Ala Arg Gln Gln Asp Ala Met
85 90 95
Glu Ser Asn Phe Glu Phe Val Glu Ser Arg Arg Met Ile Gly Leu Met
100 105 110
Arg Asp Asp Val Ala Ala Arg Ala Leu Asp Val Leu Val Pro Leu Arg
115 120 125
His Ala Ala Trp Gly Ala Asn Met Asn Asn Ala Gln Ile Cys Ala Leu
130 135 140
Gly Tyr Gly Thr Val Phe Thr Ala Pro Ala Met Phe His Ala Met Asp
145 150 155 160
Asn Leu Gly Val Ala Gln Tyr Leu Thr Arg Leu Ala Leu Ala Met Ala
165 170 175
Glu Pro Asp Val Leu Glu Ala Ala Lys Ala Thr Trp Thr Arg Asp Ala
180 185 190
Ala Trp Gln Pro Leu Arg Arg Tyr Val Glu Asp Thr Leu Val Val Ala
195 200 205
Asp Pro Val Glu Leu Phe Ile Ala Gln Asn Leu Ala Leu Asp Gly Leu
210 215 220
Leu Tyr Pro Leu Val Tyr Asp Arg Phe Val Asp Glu Arg Ile Ala Leu
225 230 235 240
Glu Gly Gly Ser Ala Val Ala Met Leu Thr Ala Phe Met Pro Glu Trp
245 250 255
His Thr Glu Ser Asn Arg Trp Ile Asp Ala Val Val Lys Thr Met Ala
260 265 270

1
Cont

Ala Glu Ser Asp Asp Asn Arg Ala Leu Leu Ala Arg Trp Thr Arg Asp
275 280 285
Trp Ser Ala Arg Ala Glu Ala Ala Leu Ala Pro Val Ala Ala Arg Ala
290 295 300
Leu Gln Asp Ala Gly Arg Ala Ala Leu Asp Glu Val Arg Glu Gln Phe
305 310 315 320
His Ala Arg Ala Ala Arg Leu Gly Ile Ala Leu
325 330

<210> 4
<211> 89
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomM polypeptide

<400> 4
Met Ser Asn Val Phe Ile Ala Phe Gln Ala Asn Glu Asp Ser Arg Pro
1 5 10 15
Ile Val Asp Ala Ile Val Ala Asp Asn Pro Arg Ala Val Val Val Glu
20 25 30
Ser Pro Gly Met Val Lys Ile Asp Ala Pro Asp Arg Leu Thr Ile Arg
35 40 45
Arg Glu Thr Ile Glu Glu Leu Thr Gly Thr Arg Phe Asp Leu Gln Gln
50 55 60
Leu Gln Val Asn Leu Ile Thr Leu Ser Gly His Ile Asp Glu Asp Asp
65 70 75 80
Asp Glu Phe Thr Leu Ser Trp Ser His
85

W
Cont
<210> 5
<211> 516
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomN polypeptide

<400> 5
Met Asp Thr Pro Thr Leu Lys Lys Lys Leu Gly Leu Lys Asp Arg Tyr
1 5 10 15

Ala Ala Met Thr Arg Gly Leu Gly Trp Glu Thr Thr Tyr Gln Pro Met
 20 25 30
 Asp Lys Val Phe Pro Tyr Asp Arg Tyr Glu Gly Ile Lys Ile His Asp
 35 40 45
 Trp Asp Lys Trp Val Asp Pro Phe Arg Leu Thr Met Asp Ala Tyr Trp
 50 55 60
 Lys Tyr Gln Gly Glu Lys Glu Lys Leu Tyr Ala Val Ile Asp Ala
 65 70 75 80
 Phe Thr Gln Asn Asn Ala Phe Leu Gly Val Ser Asp Ala Arg Tyr Ile
 85 90 95
 Asn Ala Leu Lys Leu Phe Leu Gln Gly Val Thr Pro Leu Glu Tyr Leu
 100 105 110
 Ala His Arg Gly Phe Ala His Val Gly Arg His Phe Thr Gly Glu Gly
 115 120 125
 Ala Arg Ile Ala Cys Gln Met Gln Ser Ile Asp Glu Leu Arg His Tyr
 130 135 140
 Gln Thr Glu Thr His Ala Met Ser Thr Tyr Asn Lys Phe Phe Asn Gly
 145 150 155 160
 Phe His His Ser Asn Gln Trp Phe Asp Arg Val Trp Tyr Leu Ser Val
 165 170 175
 Pro Lys Ser Phe Phe Glu Asp Ala Tyr Ser Ser Gly Pro Phe Glu Phe
 180 185 190
 Leu Thr Ala Val Ser Phe Ser Phe Glu Tyr Val Leu Thr Asn Leu Leu
 195 200 205
 Phe Val Pro Phe Met Ser Gly Ala Ala Tyr Asn Gly Asp Met Ser Thr
 210 215 220
 Val Thr Phe Gly Phe Ser Ala Gln Ser Asp Glu Ser Arg His Met Thr
 225 230 235 240
 Leu Gly Ile Glu Cys Ile Lys Phe Leu Leu Glu Gln Asp Pro Asp Asn
 245 250 255
 Val Pro Ile Val Gln Arg Trp Ile Asp Lys Trp Phe Trp Arg Gly Tyr
 260 265 270
 Arg Leu Leu Thr Leu Val Ala Met Met Met Asp Tyr Met Gln Pro Lys
 275 280 285
 Arg Val Met Ser Trp Arg Glu Ser Trp Glu Met Tyr Ala Glu Gln Asn
 290 295 300
 Gly Gly Ala Leu Phe Lys Asp Leu Ala Arg Tyr Gly Ile Arg Glu Pro
 305 310 315 320
 Lys Gly Trp Gln Asp Ala Cys Glu Gly Lys Asp His Ile Ser His Gln
 325 330 335
 Ala Trp Ser Thr Phe Tyr Gly Phe Asn Ala Ala Ser Ala Phe His Thr
 340 345 350
 Trp Val Pro Thr Glu Asp Glu Met Gly Trp Leu Ser Ala Lys Tyr Pro
 355 360 365

Asp Ser Phe Asp Arg Tyr Tyr Arg Pro Arg Phe Asp His Trp Gly Glu
370 375 380
Gln Ala Arg Ala Gly Asn Arg Phe Tyr Met Lys Thr Leu Pro Met Leu
385 390 395 400
Cys Gln Thr Cys Gln Ile Pro Met Leu Phe Thr Glu Pro Gly Asn Pro
405 410 415
Thr Lys Ile Gly Ala Arg Glu Ser Asn Tyr Leu Gly Asn Lys Phe His
420 425 430
Phe Cys Ser Asp His Cys Lys Asp Ile Phe Asp His Glu Pro Gln Lys
435 440 445
Tyr Val Gln Ala Trp Leu Pro Val His Gln Ile His Gln Gly Asn Cys
450 455 460
Phe Pro Pro Asp Ala Asp Pro Gly Ala Glu Gly Phe Asp Pro Leu Ala
465 470 475 480
Ala Val Leu Asp Tyr Tyr Ala Val Thr Met Gly Arg Asp Asn Leu Asp
485 490 495
Phe Asp Gly Ser Glu Asp Gln Lys Asn Phe Ala Ala Trp Arg Gly Gln
500 505 510
Ala Thr Arg Asn
515

Aut Cmt

<210> 6
<211> 118
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomO polypeptide

<400> 6
Met Ala Val Ile Ala Leu Lys Pro Tyr Asp Phe Pro Val Lys Asp Ala
1 5 10 15
Val Glu Lys Phe Pro Ala Pro Leu Leu Tyr Val Cys Trp Glu Asn His
20 25 30
Leu Met Phe Pro Ala Pro Phe Cys Leu Pro Leu Pro Pro Asp Met Pro
35 40 45
Phe Gly Ala Leu Ala Gly Asp Val Leu Pro Pro Val Tyr Gly Tyr His
50 55 60
Pro Asp Phe Ala Lys Ile Asp Trp Asp Arg Val Glu Trp Phe Arg Ser
65 70 75 80
Gly Glu Pro Trp Ala Pro Asp Pro Ala Lys Ser Leu Ala Gly Asn Gly
85 90 95
Leu Gly His Lys Asp Leu Ile Ser Phe Arg Thr Pro Gly Leu Asp Gly

100
Leu Gly Gly Ala Ser Phe
115

105

110

<210> 7
<211> 354
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomP polypeptide

<400> 7
Met Ser His Gln Leu Thr Ile Glu Pro Leu Gly Val Thr Ile Glu Val
1 5 10 15
Glu Glu Gly Gln Thr Met Leu Asp Ala Ala Leu Arg Gln Gly Ile Tyr
20 25 30
Ile Pro His Ala Cys Cys His Gly Leu Cys Gly Thr Cys Lys Val Ala
35 40 45
Val Leu Asp Gly Glu Thr Asp Pro Gly Asp Ala Asn Pro Phe Ala Leu
50 55 60
Met Asp Phe Glu Arg Glu Glu Gly Lys Ala Leu Ala Cys Cys Ala Thr
65 70 75 80
Leu Gln Ala Asp Thr Val Ile Glu Ala Asp Val Asp Glu Glu Pro Asp
85 90 95
Ala Glu Ile Ile Pro Val Arg Asp Phe Ala Ala Asp Val Thr Arg Ile
100 105 110
Glu Gln Leu Thr Pro Thr Ile Lys Ser Ile Arg Leu Lys Leu Ser Gln
115 120 125
Pro Ile Arg Phe Gln Ala Gly Gln Tyr Val Gln Leu Glu Ile Pro Gly
130 135 140
Leu Gly Gln Ser Arg Ala Phe Ser Ile Ala Asn Ala Pro Ala Asp Val
145 150 155 160
Ala Ala Thr Gly Glu Ile Glu Leu Asn Val Arg Gln Val Pro Gly Gly
165 170 175
Leu Gly Thr Gly Tyr Leu His Glu Gln Leu Ala Thr Gly Glu Arg Val
180 185 190
Arg Leu Ser Gly Pro Tyr Gly Arg Phe Phe Val Arg Arg Ser Ala Ala
195 200 205
Arg Pro Met Ile Phe Met Ala Gly Gly Ser Gly Leu Ser Ser Pro Arg
210 215 220
Ser Met Ile Ala Asp Leu Leu Ala Ser Gly Val Thr Ala Pro Ile Thr
225 230 235 240

*1
a
cont*

Leu Val Tyr Gly Gln Arg Ser Ala Gln Glu Leu Tyr Tyr His Asp Glu
245 250 255
Phe Arg Ala Leu Ala Glu Arg His Pro Asn Phe Thr Tyr Val Pro Ala
260 265 270
Leu Ser Glu Gly Ala Pro His Ala Gly Gly Asp Val Ala Gln Gly Phe
275 280 285
Val His Asp Val Ala Lys Ala His Phe Gly Gly Asp Phe Ser Gly His
290 295 300
Gln Ala Tyr Leu Cys Gly Pro Pro Ala Met Ile Asp Ala Cys Ile Thr
305 310 315 320
Thr Leu Met Gln Gly Arg Leu Phe Glu Arg Asp Ile Tyr His Glu Lys
325 330 335
Phe Ile Ser Ala Ala Asp Ala Gln Gln Thr Arg Ser Pro Leu Phe Arg
340 345 350
Arg Val

a
WT
<210> 8
<211> 118
<212> PRT
<213> Burkholderia cepacia

<220>
<223> TomQ polypeptide

<400> 8
Met Asp Ala Gly Arg Val Cys Gly Thr Val Thr Ile Ala Gln Thr Asp
1 5 10 15
Glu Arg Tyr Ala Cys Val Ser Gly Glu Ser Leu Leu Ala Gly Met Ala
20 25 30
Lys Leu Gly Arg Arg Gly Ile Pro Val Gly Cys Leu Asn Gly Gly Cys
35 40 45
Gly Val Cys Lys Val Arg Val Leu Arg Gly Ala Val Arg Lys Leu Gly
50 55 60
Pro Ile Ser Arg Ala His Val Ser Ala Glu Glu Asn Asp Gly Tyr
65 70 75 80
Ala Leu Ala Cys Arg Val Val Pro Asp Gly Asp Val Glu Leu Glu Val
85 90 95
Ala Gly Arg Leu Arg Lys Pro Phe Phe Cys Gly Met Ala Cys Ala Gly
100 105 110
Thr Ala Ala Ile Asn Lys
115

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 9
agtccgccat ggaggcgaca ccgatcatga atcagc 36

<210> 10
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 10
caccgaccat ggatcagcac cccaccgatc ttcc 34

1
A
Cont

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 11
tgccgccttc catgggttct gccgcgaaca gcag 34

<210> 12
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 12
agcaagccat ggccatcgag ctgaagacag tcgacatca 39

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Designed PCR primer

<400> 13
ccgaccatca cctgctcggc cagatggaag tcgag 35